Metatranscriptomics Workflows & QC — Hands-on

Learn how to design and execute metatranscriptomics projects that capture active microbial functions. This module walks from study design and depletion strategies through read QC, mapping, quantification and differential expression so that you can interpret transcriptional activity in clinical, environmental and industrial microbiomes.

Metatranscriptomics Workflows & QC

Help Desk · WhatsApp

Session Index

Session 1

Fee: Rs 8800 Apply Now

Metatranscriptomics Concepts & Study Design

What metatranscriptomics measures and when to use it

- active vs potential function
- linking metagenome and metatranscriptome
- clinical, environmental and bioprocess contexts

Experimental design for metatranscriptomics

- time series and perturbation studies
- replicates and blocking
- RNA stabilisation and extraction considerations

Library types and strandedness choices

strand specific protocols polyA vs total RNA in host associated samples read length and depth planning

Session 2

Fee: Rs 11800 Apply Now

Read QC, Host & rRNA Depletion

Metatranscriptomics specific read QC

quality and adapter trimming over represented sequences RNA degradation signatures

Host read removal for microbiome expression

mapping to host genome ethics and privacy in host associated data balancing stringency and sensitivity

rRNA depletion in wet lab and in silico

rRNA removal kits overview in silico rRNA filtering evaluating depletion efficiency

Session 3

Fee: Rs 14800 Apply Now

Mapping, Quantification & Differential Expression

Reference choices and mapping strategies

mapping to MAGs and reference genomes pseudoalignment vs full alignment multi mapping reads and ambiguity

Quantification and normalisation options

count matrices and TPM library size and composition biases linking to functional databases KEGG and eggNOG

Differential expression and visualisation

DESeq2 and edgeR style models MA plots and volcano plots pathway level summaries

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: Metatranscriptome Report from Real Dataset

End to end metatranscriptomics workflow

theory plus guided practical

Summarising active functions and pathways

heatmaps and pathway activity plots linking expression to taxa or MAGs context with resistome and metagenome modules

Deliverables: pipeline outline, result tables and report

counts and normalised matrices R or Python notebook PDF or HTML summary for stakeholders